REMARKS

Claim 1 was pending in the instant application and has now been cancelled without prejudice. New claims 32-50 have been added and thus are pending. Support for the new claims can be found in the specification and in the claims of the parent applications as originally filed.

The title has been amended to more clearly reflect the subject matter being claimed. Applicants submit herewith a "VERSION WITH MARKINGS TO SHOW CHANGES MADE", set forth as Appendix A, indicating the specific amendments made to the title.

Figure 1 and the Sequence Listing have been amended to delete the initial proline residue from the minimal VP16 domain shown in Figure 1 and the Sequence Listing, as this initial proline residue is not derived from the VP16 sequence. Support for this amendment may be found, for example, at page 29, lines 18-20, which states that the minimal activation domains of the invention were derived from VP16 and comprise positions 436 to 477 according to Seipel et al. Seipel et. al. is incorporated into the specification in its entirety at page 28, lines 30-32. This reference teaches the amino acid sequence of the entire VP16 molecule and utilizes the same numbering system for the amino acid residues as is used in the instant specification. One of ordinary skill in the art would be able to determine from Seipel et al. that the initial proline shown in Figure 1 as originally filed and in the Sequence listing prior to amendment is not derived from VP16; residue 435 of VP16 is a histidine. The proline residue was generated when constructing the vector surrounding the VP16 minimal domain; one skilled in the art would be cognizant of the fact that this initial proline derived from the cloning method used and that other amino acids could alternatively be positioned upstream of the alanine according to the desired restriction site or linker region in the surrounding vector. For example, the specification at page 30, lines 4-5, states that "[t]he protruding 5' ends of the double stranded oligonucleotides are compatible with the cleavage site of restriction endonuclease XmaI." It would be readily apparent to the ordinary skilled artisan that other restriction sites could be used for cloning depending on the vector chosen, in which case the 5' ends of the oligonucleotides would differ, leading potentially to a different amino acid residue from proline upstream of Ala-436 of VP16. The correct

sequence for VP16 positions 436 to 447 begins at the alanine residue shown in amended Figure 1 and in the amended sequence listing.

In accordance with 37 C.F.R. §1.82, Applicants submit herewith substitute pages 38-43 which contain a revised Sequence Listing for the parent application that complies with the sequence listing rules and that recites the correct amino acid sequence for VP16 positions 436-477. Applicants have also amended the specification to include substitute pages 38-43 and have requested renumbering of the pages accordingly.

No new matter has been added to the claims or specification.

CONCLUSION

All pending claims are believed to be in condition for allowance. If a telephone conversation with Applicants' Attorney would expedite the prosecution of the above-identified application, the examiner is urged to call Applicants' Attorney at (617) 227-7400.

Respectfully submitted,

LAHIVE & COCKFIELD, LLP

Date: **August 3, 2001**

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APPENDIX A

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Please amend the title as follows:

Transgenic Organisms Having Transcriptional Activators With Graded Transactivation Potential